

Section A

Describe the Physics of Superposition/Convolution Method of Dose Calculation used in Modern Treatment Planning System (TPS) Algorithms.

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1.0 Introduction

The goal of radiation therapy is to deliver a dose of radiation to a tumour in a patient, while keeping the dose to surrounding healthy tissue as low as possible. This is done via a series of external radiation beam dose fractions from a linear accelerator that intersects and concentrates on the tumour travelling through a variety of different paths. Ideally the treatment volume would exactly match the 3D tumour volume, delivering exactly zero dose to surrounding healthy tissue, but in practice this is not possible, so dose calculations have to be carried out in 3D, in order for the distribution of radiation to be found and the most effective treatment can be administered. A crucial component of the treatment planning process is the accuracy of the dose distribution calculations. The most effective treatments would deliver at least 95% of the dose to the tumour volume, with a minimum precision of $\pm 5\%$ in uniformity of the radiation beam. Without a detailed knowledge of this distribution the radiation administered could cause more damage to the patients. Modern treatment planning systems (TPS) aim to determine the dose distribution by accounting for the effects of attenuation by the tissue and heterogeneities on the administered radiation by utilising one of a number of algorithms methods. Presently, for photons, the superposition/convolution algorithms are considered to be the most accurate and widely used methods of dose calculation, short of performing a lengthy monte-carlo simulation.

2.0 Superposition / Convolution Method

There are two main ways of calculating the dose and its distribution given to a patient. A data-driven method is based on previous measurements being stored in large data tables at given depths and positions on a three-dimensional grid. The algorithm is employed by determining the dose through extrapolation, but its drawback is the need for storing large amounts of data in tables. The second method is model-driven and involves solving algorithms from first principles. The photons eventually reaching the patient are modelled from their creation by electrons in the accelerator, but require a large amount of calculations and are very time consuming. The best dose distribution

methods are therefore a compromise between the lengthy calculations and large amounts of data storage, incorporating a little of both to get the most accurate results at the fastest speed possible.

The superposition / convolution method allows a 3D calculation to be carried out, which intrinsically handles the effects of patient heterogeneities on both primary and scattered radiation. Rather than correcting for measured dose distributions, the superposition / convolution algorithm computes dose distributions from first principles. The calculation consists of four parts:

- Modelling the incident energy fluence as it exits the accelerator
- Projection of the energy fluence through the density representation of a patient to compute a TERMA volume
- 3D superposition of an energy deposition kernel
- Electron contamination model

2.1 Energy Fluence

The incident energy fluence distribution is modelled as a two-dimensional array which describes the intensity of the radiation exiting the linear accelerator. This array can be adjusted to account for filters and beam modifiers such as blocks and wedges, which shape the beam (figure 1).

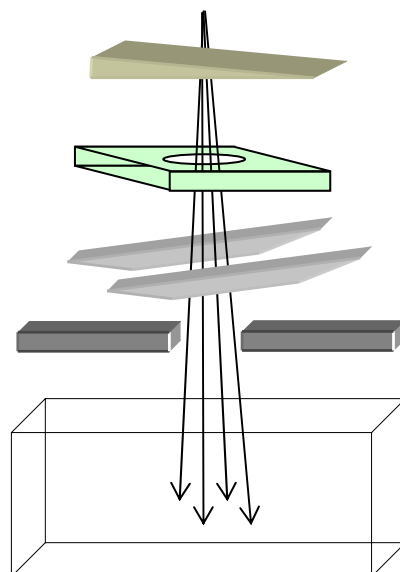


Figure 1. Distribution of beam is modelled accounting for wedges and filters along with variations of beam intensity across patient surface [1]

2.2 Projection of Energy Fluence

The incident energy fluence is projected through a CT image and attenuated using mass attenuation coefficients stored in lookup tables as a function of density and radiological depth and taking into account patient heterogeneities. A TERMA (Total energy released per unit mass) volume is calculated using ray-tracing techniques from the attenuated beam. Since the fluence at a given point cannot be mono-energetic due to absorption and scattering, the energy fluence is calculated in small differentials, so TERMA is the sum of all the terms components as a function of photon energy and distance:

$$T(E, r) = \frac{\mu(E)}{\rho} \psi(E, r) \quad \text{Equation 1}$$

where: $\frac{\mu}{\rho}$ = mass attenuation coefficient

ψ = energy fluence

The unattenuated energy fluence emanating from the linear accelerator (linac) is known, however, the differential energy fluence function as it is attenuated and modified in the material cannot be measured exactly, so monte-carlo simulations are used to obtain the distribution from approximations calculated from measured fluences at the position of interest.

2.3 Superposition of Deposition Kernel

Superposition allows the spread of a number of functions to be predicted by superimposing the responses of the individual functions. In dose calculations the aim is to find the response (TERMA) to a dose deposition (KERMA – Kinetic energy released per unit mass) in the patient. The three-dimensional dose distribution in the patient is computed by the superposition of the absorbed dose values at the point of interest from the knowledge of TERMA with respect to the dose deposition kernel. The kernel represents the spread of energy from the primary photon interaction point through the TERMA volume. The kernel is energy dependent, but to carry out the calculations in energy differential form would be too computationally expensive. A

good simplification is to represent the spectrum of dose deposition kernels in terms of the ratio of KERMA to TERMA and separating the primary contribution from the scattered component. This produces a good representation of the effect of spectral differences, whilst reducing the calculation to produce the spectral dependent kernel.

2.4 Electron contamination

Although the primary source of dose to the patient is through photons, contamination from electrons is significant to the dose near the surface of the TERMA volume. The electron dose contribution is accounted for in the algorithm by modelling a photon only dose and comparing it to the measured dose at shallow depths. This effect is then modelled with an exponential fall-off through the depth of the irradiated mass.

2.5 Convolution

Once the TERMA and deposition kernel are known for every calculation point, convolution is carried out to find the distribution of dose through the patient. Convolution is a mathematical process that combines two functions in a particular way to produce a third function. One of the input functions is the convolution kernel, or spread function (the energy deposition kernel in this case), and the two input functions are said to be convolved.

In radiation therapy the dose distribution in the patient is the function of interest, and is obtained using knowledge of the energy deposition kernel and TERMA. However, the TERMA calculation is fairly complex due to the energy fluence, requiring a lengthy method from the back projection of the energy kernel through the patient to deduce the function. Once this is known, the convolution method can be employed, which evaluates an integral that expresses the amount of overlap of the two input functions as the energy deposition kernel is shifted over the TERMA volume, therefore blending one function with the other. The convolution of two functions is given by:

$$h(x) = f(x)g(x) = \int f(\tau)g(x-\tau)d\tau = \int g(\tau)f(x-\tau)d\tau \quad \text{Equation 2}$$

where: $f(x)g(x)$ denotes convolution of f and g .

A convolution at a particular point, x , is evaluated by positioning each element of the kernel ($g(x)$), and centring it at that point. The corresponding elements of the two functions (TERMA at x , and the kernel element at the same point) are multiplied together and all the products summed together to obtain a single element of the output function. Convolution at the neighbouring points is then obtained by shifting the kernel, so it is centred at all the relevant points in the input TERMA function and repeating the multiplication and addition process until all elements of the output dose distribution function are obtained.

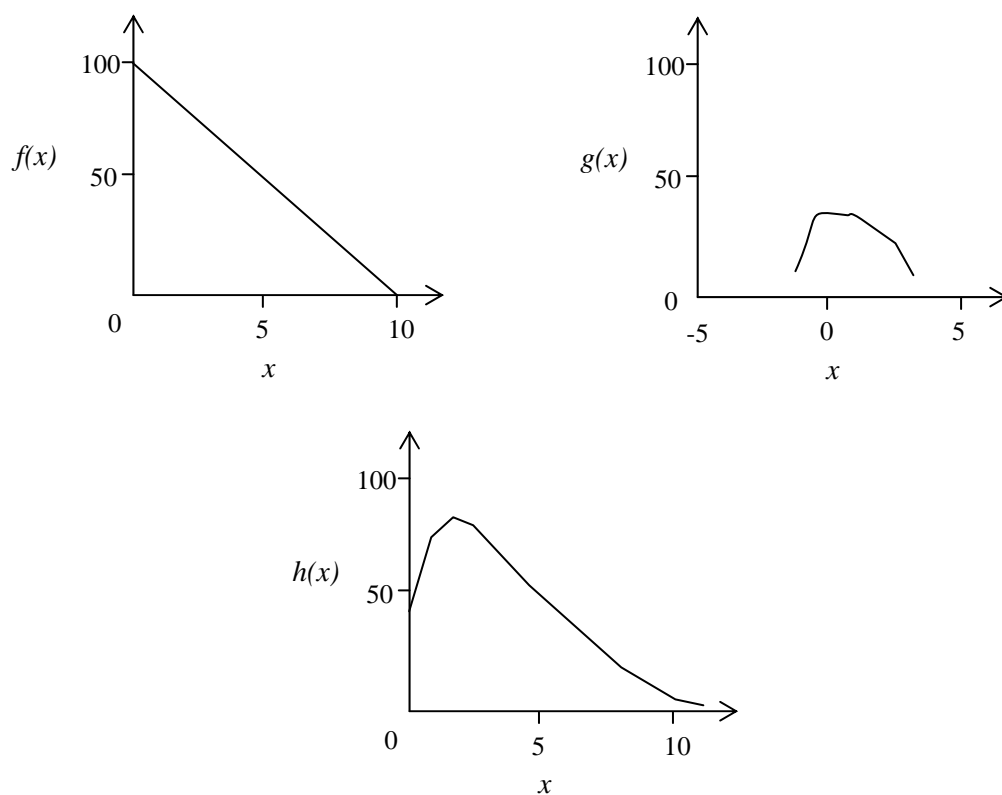


Figure 2. A convolution function from two functions where $g(x)$ is the kernel [1]

This convolution method is important in both medical imaging and radiation therapy for a variety of reasons. If the response of a system to a point object (impulse response) is known, and the system obeys certain assumptions, the response of the system to an arbitrary object can be determined.

2.6 Assumptions made in superposition/convolution algorithms

The aim of any treatment planning system method is to get as close to the actual physical situation as possible so that the most effective method of treatment can be implemented. Due to the nature of the functions involved and the amount of calculations required to obtain an accurate picture, approximations and assumptions must be made to simplify these calculations. Dose distribution algorithms require data from measured attributes on which to base their calculations. This produces limitations on the boundaries of the measured data that is stored. Any information that is required beyond a boundary must be extrapolated, and there is no guarantee that this process will be an accurate representation of the true function. The input data usually only covers a limited range of depths and field sizes within the patient, so in any particular situation, approximations are made by linear interpolations between data points.

Another assumption is that the radiation emanates from a point source. In reality this source has a finite size, with a significant contribution to the photon beam from Compton scatters. This is accounted for in the energy fluence with a Gaussian function. Also, the radiation entering the patient from the beam is assumed to be parallel, although the non-uniformity of the intensity is accounted for.

2.7 Strengths and weaknesses

There are many other algorithms that can be used to calculate dose distributions for treatment planning, including 3D Fast Fourier Transforms, Monte-Carlo simulations and pencil beam methods. All of these are model based algorithms, which differ from the superposition/convolution algorithm by the fact that they do not use the superposition technique in the convolution process.

While the FFT (fast fourier transform) techniques are much faster processes, they require the assumption of a spatially invariant kernel. Accurate calculations can therefore only be performed in a material whose density is homogeneous. This significantly reduces the accuracy of the computation because it ignores the effects of

inhomogeneities. The pencil beam method bases its algorithm on previously measured dose distributions in a phantom, such as water. Water gives a good approximation to soft tissue for modelling purposes, but proves to be inaccurate in the presence of inhomogeneities due to variations in electron densities. Monte-carlo simulations can be used directly to measure dose distribution in a patient entirely from first principles. This would provide highly accurate three-dimensional information about the distribution in the patient, accounting for complex geometries and inhomogeneities, however, a huge disadvantage is the amount of computational resources and time required to calculate each distribution.

Although the superposition/convolution algorithm has its advantages over the other methods discussed above, there are some weaknesses in the algorithm calculation. At present, an additional error margin of several centimetres is added to the computed treatment volume as it is essential that the entire volume of the tumour be treated in each dose fraction. The calculation is only an approximation anyway (although a very good one), but the extra margin allows for patient motion and inaccuracies in repositioning the patient for each treatment session. This is not an ideal situation because, as the margin increases, more healthy tissue is exposed, which ultimately limits the radiation dose that can be delivered to the tumour. Many of the other weaknesses have been previously discussed.

3.0 Conclusion

Treatment planning system algorithms form a crucial part of radiation therapy for dose distribution calculations to patients. There are a number of approaches that can be taken, involving the use of measured data from phantoms and previous calculations along with models based on first-principle physics. Currently the favoured method is the superposition/convolution algorithm, which utilises some of the best data and modelling techniques available to produce accurate dose distributions, accounting for a number of complexities and inhomogeneities in the human body, along with being able to represent the use of wedges and multi-leaf collimators to shape and direct the photon beam. Although this calculation method can present a relatively accurate picture of the true distribution of dose in the patient, due to the nature of use for these

algorithms and the necessity to be as accurate as possible, it is thought that as computational speed and power increase, the Monte-Carlo simulations will form a more integral part of the calculations.

4.0 References

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